

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 18:49:41 ; Search time 290 Seconds  
(without alignments)  
8099.428 Million cell updates/sec

Title: US-09-807-933B-13

Perfect score: 1043

Sequence: 1 ggatcctgggacaagatgaa.....cgcaagtaaacgagatgcc 1043

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_101002.\*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1043	100.0	1043	21	AAA62732
2	1043	100.0	1043	24	AAA43250
3	594.6	57.0	1017	21	AAA62726
4	594.6	57.0	1017	24	AAA43244
5	421.2	40.4	1101	21	AAA62727
6	421.2	40.4	1101	24	AAA43245
7	362.4	34.7	1083	21	AAA62728
8	362.4	34.7	1083	24	AAA43246
9	333.8	32.0	1041	21	AAA62731

10	333.8	32.0	1041	24	AA143249	Phycomyces nitens
11	288.4	27.7	1017	21	AAA62729	Endoglucanase nucl
12	288.4	27.7	1017	24	AA143247	Rhizopus arrhizus
13	286.4	27.5	1058	13	AAQ26405	Humicola insolens
14	286.4	27.5	1060	12	AAQ14856	Humicola insolens
15	286.4	27.5	1060	13	AAQ26380	Endoglucanase #1.
16	286.4	27.5	1060	13	AAQ25932	Cellulase containe
17	286.4	27.5	1060	13	AAQ29934	Endoglucanase gene
18	286.4	27.5	1060	13	AAQ30067	Sequence encoding
19	286.4	27.5	1060	14	AAQ41732	Dye transfer inhib
20	286.4	27.5	1060	14	AAQ49941	Endoglucanase enzy
21	286.4	27.5	1060	16	AAZ60178	H. insolens endogl
22	286.4	27.5	1060	17	AA10182	Alkaline endogluc
23	286.4	27.5	1060	19	AAV15072	Humicola insolens
24	286.4	27.5	1060	19	AAV15065	Humicola insolens
25	286.4	27.5	1060	21	AAAS3334	Endoglucanase nucl
26	284.8	27.3	807	19	AAV16104	Humicola insolens
27	283.4	27.2	1164	21	AAA62730	Endoglucanase nucl
28	283.4	27.2	1164	24	AA143248	Rhizopus arrhizus
29	281.6	27.0	1060	13	AAQ30072	43kD endoglucanase
30	280	26.8	1060	13	AAQ31181	H. insolens cellul
31	274.8	26.3	927	17	AA139062	Chimeric endogluc
32	273.4	26.2	894	17	AA139061	Chimeric endogluc
33	273.4	26.2	960	17	AA139047	CDNA encoding cell
34	271.8	26.1	922	19	AAV15076	Hybrid DNA compris
35	268.2	25.7	925	19	AAV15076	Hybrid DNA compris
36	262.2	25.1	672	24	AA143263	Humicola insolens
37	262.2	25.1	672	24	AA169425	Humicola insolens
38	260.2	24.9	1174	17	AA139050	CDNA encoding cell
39	260.2	24.9	1174	19	AAV39096	Monocomponent endo
40	257.4	24.7	922	19	AAV15073	Hybrid DNA compris
41	247.8	23.8	1261	19	AAV23748	Humicola grisea ce
42	246.2	23.6	1132	17	AA139053	CDNA encoding cell
43	240.2	23.0	913	17	AA139051	CDNA encoding cell
44	237.8	22.8	885	17	AA139075	Chimeric endogluc
45	235.4	22.6	1473	12	AAQ14857	Fusarium oxysporum

#### ALIGNMENTS

RESULT 1  
AAA62732  
ID AAA62732 standard; DNA; 1043 BP.  
XX  
AC AAA62732;  
XX  
XX 25-SEP-2000 (first entry)  
DE Endoglucanase nucleotide sequence 7.  
XX  
DE Endoglucanase; cellulose breakdown; produce pulp; papermaking;  
KW animal foodstuff; ss.  
XX  
OS Rhizopus oryzae.  
XX  
PN WO200024879-A1.  
XX  
PD 04-MAY-2000.  
XX  
PF 25-OCT-1999; 99WO-JP05884.  
XX  
PR 23-OCT-1998; 98JP-0302387.  
XX  
PA (MEIJU) MEIJI SEIKA KAISHA LTD.  
XX  
PI Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;  
PI Murashima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;  
XX  
DR WPI; 2000-365117/31.  
XX  
PT Endoglucanases of fungal origin with high activity under alkaline  
PT conditions for production of paper pulp and animal feedstuffs -









Wed Jun 18 17:55:18 2003

OS	Rhizopus arrhizus.
XX	WO200242474-A1.
XX	PNP
XX	30-MAY-2002.
PD	
XX	21-NOV-2001; 2001WO-JP10188.
PP	
XX	21-NOV-2000; 2000JP-0354296.
XX	(MEIJI) MEIJI SEIKA KAISHA LTD.
PA	
XX	Nakane A, Baba Y, Koga J, Kubota H;
PI	
XX	WPI; 2002-471729/50.
DR	P-PSDB; AMO15053.
XX	
XX	Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
PT	with effect of endoglucanase activity enhanced in processing fibers,
PT	deinking waste paper and improving freeness of paper pulp
PT	-
XX	Disclosure; Page 60-63; 109pp; Japanese.
PS	
XX	The invention comprises the amino acid and coding sequences of
XX	Zygomycetes-originated endoglucanase enzymes lacking the cellulose
CC	binding domain. The zygomycetes-originated endoglucanase enzymes of the
CC	invention have enhanced endoglucanase activity. The zygomycetes-
CC	originated endoglucanase enzymes of the invention are useful for
CC	processing fibres, de-inking waste paper and improving the freshness of
CC	paper pulp - which is particularly applicable in detergent compositions.
CC	The present DNA sequence represents an endoglucanase-related gene
CC	sequence of the invention.
XX	
XX	Sequence 1101 BP; 268 A; 258 C; 257 G; 318 T; 0 other;
SQ	
	Query Match 40.4%; Score 421.2; DB 24; Length 1101;
	Best Local Similarity 72.4%; Pred. No. 4.7e-75;
	Matches 565; Conservative 0; Mismatches 203; Indels 12; Gaps 1;
QY	253 ACGCTGCCACAGAACGACCAGCGCGGTTCACAAGAAGACTACGACGGCTCCCGCC 312
DB	334 AGCAATGGCAATAAACTTCTGAAGCGGTCTATAAAGCACTACTACCACTGCTCCCGCT 393
QY	313 AAGAAGACACGACCGCTGCAGAGGTTTGACTCCGTCCAATCAGGAGCTGCTCTTCG 372
DB	394 AAGGAATTACAATACTACTGCCAAGCTTCAAACCTCTTAACCTTAGCGGC----- 444
QY	373 GGAAAGTACAGCGCTGTACGCGTGTGCGGTAGCGGCAAGCGGTCACTACCGCTACTGG 432
DB	445 ---AAATACTCCATTGTCTCTGTGTGTGCTCTGTGTAACGGGTCTACTACTCTGTTATGG 501
QY	433 GACTGTGCAAGGCTTCTGCTCTGTGCGCGGCAAGGCTAAAGTCAAGCTCGCTGCTCAAG 492
DB	502 GATTGCTGTAAAGGCTTCTGTAGCTGGCCGGTAAAGGCAATGTCAAGTTCTCTGCTCAAG 561
QY	493 TCCTGCAACAGGAAGCGGCTCACCGCTTTAGGCACTCCAAAGCCAGTCCGCTGTCAC 552
DB	562 TCCTGTAAAGAGATGGTGTCACTGCGCTTAGTGACAGCAATGTCCAAAAGTGGCTGTAA 621
QY	553 GGCGGCAACTCTCATGTGCAAGCAACAGCGCATGGCTCTCAACGACACCACTTGTCT 612
DB	622 GGTGTAACAGTTATCATGTGTAAAGCAACACAGCTTGGCTGTAAACGATATCTTGCC 681
QY	613 TACGGTTTCGTGCTGCTGCAATTAGCGGGGTGGGAGAGCGCGTGGTGTCTCTCTGC 672
DB	682 TATGTTTTGCTGTCTGTGCAATCAGTGGTGGTGTGAATCTCGCTGGTCTCTTCTGT 741
QY	673 TTCGAGCTACCTTCACTTCCACAGCGTTGCTGGCAAGATGTTGCTCCAGGTCACC 732
DB	742 TTCGAACCTTACTTTCACTTCTACCTCTGTTGCTGGTAAGAAGATGGTTATCCAACTACT 801
QY	733 AACACTGGCGGTGACCTTGGCAGCTTCGACCGGTGCCCACTTCGATCTCCAGATGCCCGGC 792



```
QY 16 ATGAAGTTTCATCACTATCGCTCTCTCGGCGCTCTTGGCCCTCGCCCTTGGCACTGAGATG 75
Db |||||
QY 1 ATGAAGTTTCTTACCAATTCGCTCTCGCTATCTTGGCACTTGGCGTGGTACTGGAATG 60
Db |||||
QY 76 GCCTCCGCGCTGAGTGTCTCAAGCTCTACGGAAGTGGCGGGAAGAACTGGAACGGC 135
Db |||||
QY 61 GCCCATGCTGCTGAATGTAGCAAGGCTTACTACCAATGTGGTGAAGAACTGGGATGGA 120
Db |||||
QY 136 CCCACCTGCTGCGAGAGCGCTGACCTGCAAGTCTCGAATGAC-----TACTACAGC 189
Db |||||
QY 121 CCTACTGCTGTGAATCTGCTCTACTTGTGTTGATTAATCTGACAACTCTTCTACTCC 180
Db |||||
QY 190 CAGTGTCTGCGAGCG-----GCTCCTCGGGAACAAGTCG 225
Db |||||
QY 181 CAATGTGTTCCCAATGAAACCTCACTCCACTAACAAATCTTCTCAGAAAACCACTACT 240
Db |||||
QY 226 AGCGAGTCGCCACAGAAGACACGACCGCTGCCACAGAGAACGACGAC-----278
Db |||||
QY 241 ACTGAGAGTGCCCAAGAGACTACCACTACTAAAGGTTCCAAGAGAACCACTACTGAA 300
Db |||||
QY 279 -----CGCGCTCACAAGAGACTACGACCGCTCCGCGC 312
Db |||||
QY 301 GCCTCTAAGAGACCACTACTGAAGCTTCCAGAGACCACTACTGAAGCTCT 350
Db |||||
QY 313 AAGAAGACCAACCGCTCGCAAGGCTTCGACTCCGTCCTCAACTCGAGAGCTCGTCTTCG 372
Db |||||
QY 361 AAGAAGACCACTACTACTAAGAGGCTTCTACCTCCACTTCTCTCTCTCTCTCTCT 420
Db |||||
QY 373 G-----GAAAGTACAGCGTGTACAGCGTGGCGCTAGCGGCAACCGCGTCACTACCGC 426
Db |||||
QY 421 GCTTCTACAACTACTCCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db |||||
QY 427 TACTGGAGTGTCTGCAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 486
Db |||||
QY 481 TACTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db |||||
QY 487 GTCAAGTCTCTGCAACAGAGCGCGTCAACCGCTCTTAGCGACTTCAACGCGCACTCGCG 546
Db |||||
QY 541 GTTGGCTCTGTAAAGAGTGG---TNAGACTTCTTGTGATTAACAACACTCAAAAGCGC 597
Db |||||
QY 547 TGAACAGCGCGCAACTCTTACATGTGCAACGCAACAGCCATGGGTGTCAACGCAAC 606
Db |||||
QY 598 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
Db |||||
QY 607 CTTCGCTTACGTTTCTGCTGCGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
Db |||||
QY 658 CTTCGCTTACGTTTCTGCTGCGTGTCTTCAATTTCTGTGTGTGTGTGTGTGTGTGTGT 717
Db |||||
QY 667 TCTGTCTTACGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 726
Db |||||
QY 718 GCCTGTTTCAACTCACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 777
Db |||||
QY 727 GTCAACCAACTCGCGGTGACCTTGGCAGCTGACCGGTGCGCCACTTTCGATCTCCAGAT 786
Db |||||
QY 778 GTAAACCAACTCGGTGTTGACCTTGGCTTAAACACTGGTGTCTCACTTTCGACTTTCG 837
Db |||||
QY 787 CCGCGGCGGCGCTCGCAGTCTTCAACGATGCTCGTCCAGTGGGCGCTCCCAACGAC 846
Db |||||
QY 838 CCGCGGCGGCGCTCGCAGTCTTCAACGATGCTCGTCCAGTGGGCGCTCCCAACGAT 897
Db |||||
QY 847 GGTGGGCGCTCGCGGTACGCGCGGCTCAGCTCGCGCGGCTCGTCTCGTCTCCCGCAGC 906
Db |||||
QY 898 GGTGGGCGTCAAGATACGCGGCTGTTTCTTCTGCTCTGACTGTCTTAACCTTCTTCT 957
Db |||||
QY 907 GCCTTCAGCGCGGTGCAAGTGGCGTTCGAATGTTTCAAGTTCGAAGAACCGCGCAAC 966
Db |||||
QY 958 GCCCTTCAAGCTGGTTGTAAGTGAGATTGCGGCTGGTTCAAAACGCTGATAACCCCAAC 1017
Db |||||
QY 967 ATGACCTACAGAGGTCACTGCGCCCAAGAGATCAACCGCTAAGACCGGATCTCGCGC 1026
Db |||||
QY 1018 ATGACCTACAAACAAGTTACTCTGTCCAAGGCTATCACTGSCCAAGTCTGGCTTCAAGA 1077
Db |||||
QY 1027 AAGTAA: 1032
```

Db ||||| 1078 AATAA 1083

## RESULT 8

AAL43246  
ID AAL43246 standard; DNA; 1083 BP.

XX AC AAL43246;

XX DT 22-AUG-2002 (first entry)

XX DE Rhizopus arrhizus endoglucanase-related coding sequence 3.

XX KW Zymomyces-originated endoglucanase; cellulose binding domain;  
KW fibre processing; waste paper de-inking; paper pulp; ds, gene.

XX OS Rhizopus arrhizus.

XX PN WO200242474-A1.

XX PD 30-MAY-2002.

XX PF 21-NOV-2001; 2001WO-JP10188.

XX PR 21-NOV-2000; 2000JP-0354296.

XX PA (MEIJ ) MEIJI SEIKA KAISHA LTD.

XX PI Nakane A, Baba Y, Koga J, Kubota H;

XX DR WPI: 2002-471729/50.  
P-PSDB; AA015054.XX PT Cellulose-binding domain-lacking Zymomyces-originated endoglucanase,  
with effect of endoglucanase activity enhanced in processing fibers,  
deinking waste paper and improving freeness of paper pulp -

XX PS Disclosure; Page 65-68; 109pp; Japanese.

XX SQ The invention comprises the amino acid and coding sequences of  
CC zymomyces-originated endoglucanase enzymes lacking the cellulose  
CC binding domain. The zymomyces-originated endoglucanase enzymes of the  
CC invention have enhanced endoglucanase activity. The zymomyces-  
CC originated endoglucanase enzymes of the invention are useful for  
CC processing fibres, de-inking waste paper and improving the freeness of  
CC paper pulp - which is particularly applicable in detergent compositions.  
CC The present DNA sequence represents an endoglucanase-related gene  
CC sequence of the invention.

SQ Sequence 1083 BP; 260 A; 297 C; 231 G; 295 T; 0 other;

Query Match 34.7%; Score 362.4; DB 24; Length 1083;

Best Local Similarity 62.9%; Pred. No. 2.5e-63;

Matches 683; Conservative 0; Mismatches 331; Indels 72; Gaps 5;

QY 16 ATGAAGTTTCATCACTATCGCTCTCTCGGCGCTCTTGGCCCTCGCCCTTGGCACTGAGATG 75

Db 1 ATGAAGTTTCTTACCATTGCTCTCCCTCTTCTGGCACTTGGCGTGGTACTGAAATG 60

QY 76 GCCTCCGCGCGCTGAGTGTCTCAAGCTCTACGGACAGTGGCGGGAAGAACTGGAACGGC 135

Db 61 GCCCATGCTGCTGAATGTAGCAAGGCTTACTACCATGTGGTGAAGAACTGGGATGGA 120

QY 136 CCCACCTGCTGCGAGAGCGGCTGACCTGCAAGTCTCGAATGAC-----TACTACAGC 189

Db 121 CCTACCTGCTGTAATCTGGCTCTACTTGGTTGATTATCTCTGACAATCTTCTTACTCC 180

QY 190 CAGTGTCTCGGAGCG-----GCTCCTCGGGAACAAGTCG 225

Db 181 CAATGTGTCTCCCAATGAAAACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 240

QY 226 AGCGAGTCGGCCCAAGAGAACCGAGCGCTGCGCCCAAGAGAACCGAGC-----278









Query Match 27.5%; Score 286.4; DB 13; Length 1058;  
Best Local Similarity 70.7%; Pred. No. 3.5e-48;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGGTCTACTACCGCTACTGGGACTGCT 439  
47 CCGCCCTGCGCGGTGTGGCGCTTGGCGCTGATGCGAGGTCCACCGCTACTGGGACTGCT 106  
440 GCAAGGCTTCGTGCTCGTGGCGCGCAAGGCTTCAACGAGCAACCTTGTCTTACG 616  
107 GCAAGGCTTCGTGCTCGTGGCGCTTGGCGCTGATGCGAGGTCCACCGCTACTGGGACTGCT 166  
500 ACAAGGAGCGGTACCGCTTGTAGCGATCCAAAGCGGAGTCCCGGCTCGCAAGTCTTACG 499  
167 AC---GCCAACTTCCAGCGTATCAGCGACTTCAGCCCAAGTCCCGGCTGGAGCGGGCG 223  
557 GCAACTCTACATGTGCAACGACAAACAGCATGCGGTGTCAACGAGCAACCTTGTCTTACG 616  
224 GTGTGCGCTTACTGTGCGCGCAACAGACCCATGGGCTGTGAACGAGACTTTCGCGCTCG 283  
617 GTTTCGCTGCGGTGCGCATTAGCGGCGGTGGCGAGCGCGCTGCTGCTGCTGCTTTCG 676  
284 GTTTTGTGCGCACCTCTATTGCGCGGCAATGAGCGGGCTGCTGCTGCGCTGCTTACG 343  
677 AGCTCAGCTTCACTTCCACGACAAACAGCATGCGGTGTCAACGAGCAACCTTGTCTTACG 736  
344 AGCTCAGCTTCACTTCCACGACAAACAGCATGCGGTGTCAACGAGCAACCTTGTCTTACG 403  
737 CTGCGGTGAGCTTGTGCGGAGTCCGCGAGCGGTGCGGAGTCCCGGCTCGCAAGTCTTACG 796  
404 CTGCGGTGAGCTTGTGCGGAGTCCGCGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 454  
797 CGCTCGGAGTCTTCAACGAGTCTGCTGCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 856  
455 GCGTGGGAGTCTTCAACGAGTCTGCTGCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 505  
857 CGCGTACGCGGAGTCCGCGAGCGGTGCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 916  
506 AGCGGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 565  
917 CGCGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 976  
566 CGCGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 625  
977 AGGAGGTCACTTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 1028  
626 GTCAGGTCCAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 677

RESULT 14  
AAQ14856  
ID AAQ14856 standard; DNA; 1060 BP.

AAQ14856;  
18-FEB-1992 (first entry)  
Humicola insolens DSM 1800 endoglucanase.

cellulase; ss.  
Humicola insolens.  
Key Location/Qualifiers  
sig\_peptide /tag= a  
mat\_peptide /tag= b  
WO9117243-A.  
14-NOV-1991.

08-MAY-1991; 91WO-DK00123.  
22-APR-1991; 91DK-0000736.  
09-MAY-1990; 90DK-0001159.  
(NOVO) NOVO NORDISK A/S.  
Rasmussen G, Mikkelsen JM, Schulein M, Patkar SA, Hagen F;  
Hjort CM, Hastrup S;  
WPI; 1991-353765/48.  
P-PSDB; AAR15271.  
Cellulase prepn. comprising endoglucanase enzyme - used in  
detergents for cellulose-contg. fabrics or to improve drainage of  
paper pulp  
Claim 11; Page 48; 67pp; English.  
The cellulase (i.e. endoglucanase) gene was isolated from a H.  
insolens cDNA library by screening with a probe based on the amino  
acid sequence of the purified enzyme.  
Sequence 1060 BP; 190 A; 377 C; 288 G; 205 T; 0 other;  
Query Match 27.5%; Score 286.4; DB 12; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 3.5e-48;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGGTCTACTACCGCTACTGGGACTGCT 439  
47 CCGCCCTGCGCGGTGTGGCGCTTGGCGCTGATGCGAGGTCCACCGCTACTGGGACTGCT 106  
440 GCAAGGCTTCGTGCTCGTGGCGCGCAAGGCTTCCGCTGCAACGAGCTGTCTTTCCTGCA 499  
107 GCAAGGCTTCGTGCTCGTGGCGCTTGGCGCTGATGCGAGGTCCACCGCTACTGGGACTGCT 166  
500 ACAAGGAGCGGTGACCGCTTGTAGCGACTCCAAAGCGGAGTCCCGGCTCGCAAGTCTTACG 556  
167 AC---GCCAACTTCCAGCGTATCAGCGACTTCAGCCCAAGTCCCGGCTGGAGCGGGCG 223  
557 GCAACTCTTACATGTGCAACGACAAACAGCATGCGGTGTCAACGAGCAACCTTGTCTTACG 616  
224 GTGTGCGCTTACTGTGCGCGCAACAGACCCATGGGCTGTGAACGAGACTTTCGCGCTCG 283  
617 GTTTCGCTGCGGTGCGCATTAGCGGCGGTGGCGAGCGCGCTGCTGCTGCTGCTGCTG 676  
284 GTTTTGTGCGCACCTCTATTGCGCGGCAATGAGCGGGCTGCTGCTGCGCTGCTTACG 343  
677 AGCTCAGCTTCACTTCCACGACAAACAGCATGCGGTGTCAACGAGCAACCTTGTCTTACG 736  
344 AGCTCAGCTTCACTTCCACGACAAACAGCATGCGGTGTCAACGAGCAACCTTGTCTTACG 403  
737 CTGCGGTGAGCTTGTGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 796  
404 CTGCGGTGAGCTTGTGCGGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 454  
797 CGCTCGGAGTCTTCAACGAGTCTGCTGCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 856  
455 GCGTGGGAGTCTTCAACGAGTCTGCTGCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 505  
857 CGCGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 916  
506 AGCGGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 565  
917 CGCGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 976  
566 CGCGTACGCGGAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 625  
977 AGGAGGTCACTTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 1028  
626 GTCAGGTCCAGTCCGCGAGTCCCGGAGTCCCGGAGTCCCGGCTCGCAAGTCTTACG 677

## RESULT 15

AAQ26380  
ID AAQ26380 standard; DNA; 1060 BP.

XX AC AAQ26380;

XX DT 07-JAN-1993 (first entry)

XX DE Endoglucanase #1.

XX KW CMC-endoase; 43 kD cellulase; monoclonal antibody; as.

XX OS Humicola insolens.

XX FH Key Location/Qualifiers

XX CDS 10..927

XX FT /\*tag= a

XX FT sig\_peptide 10..72

XX FT /\*tag= b

XX FT mat\_peptide 73..924

XX FT /\*tag= c

XX EP495257-A;

XX PN 22-JUL-1992.

XX PP 06-NOV-1991; 91EP-0202879.

XX PR 16-JAN-1991; 91EP-0870006.

XX PR 06-NOV-1991; 91EP-0202880.

XX PR 06-NOV-1991; 91EP-0202879.

XX XX (PROC ) PROCTER &amp; GAMBLE CO.

XX PI Baeck AC, Busch A, Ceulemans RAA;

XX DR WPI; 1992-243163/30.

XX DR P-PSDB; AAR26380.

XX PT Compact, granular detergent compsns. - contain high activity

XX PT cellulase and softening clay to provide synergistic effect in

XX PT softening performance

XX XX Disclosure; Page 20-21; 29pp; English.

XX CC The sequences given in AAQ26380 and AAQ26382 are endoglucanases which

XX CC are immunoreactive with a monoclonal antibody raised against a

XX CC partially purified 43 kD cellulase derived from Humicola insolens.

XX CC These endoglucanases exhibit a CMC-endoase activity of at least

XX CC about 50, pref. at least about 60, in particular at least about 90 CMC-

XX CC endoase units per mg of total protein. These endoglucanases have

XX CC molecular weight of approx. 43 kD.

XX XX Sequence 1060 BP; 190 A; 377 C; 287 G; 206 T; 0 other;

XX SQ

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

QY 557 GCAACTCTTACATGTGCAACGACAAACAGCCATGGCTGTCAACGACAAACCTTGTCTTACG 616  
 Db 224 GTGTGGCTTACTCTGTCGGCCGACACCCCATGGCTGTGAACGACGACTTCGGCTCG 283  
 QY 617 GTTTCGCTGCCCTGCCATTTAGCGCGGTGGCGAGAGCCGTGTGTCTCTCTCTCTCG 676  
 Db 284 GTTTTGTGCGCACTCTATTGCGCGCAGCAATGAGCGCGCTGGTGTCTGCGCTGTCTACG 343  
 QY 677 AGCTCACCTTCACTCCACCAGCTGTGGCAAGAGATGCTGTCCAGGTCAACCAACA 736  
 Db 344 AGCTCACCTTCACTCCAGCTGTGGCAAGAGATGCTGTCCAGGTCAACCAACA 403  
 QY 737 CTGGCGGTGACCTTGGCAGCTCGACCGGTGCCACTTCCAGATCTCCAGATGCCCGGGGCG 796  
 Db 404 CTGGCGGTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGCGGGCG 454  
 QY 797 GCGTGGGATCTTCAACCGGATCTCGTCCAGTGGGGCGCTCCCAACGACGGCTGGGGCT 856  
 Db 455 GCGTGGGATCTTCAACCGGATCTCGTCCAGTGGGGCGCTCCCAACGACGGCTGGGGCT 505  
 QY 857 GCGGTAGCGCGGATCTCGTCCAGTGGGGCGCTCCCAACGACGGCTGGGGCT 916  
 Db 506 AGCGGTAGCGCGGATCTCGTCCAGTGGGGCGCTCCCAACGACGGCTGGGGCT 565  
 QY 917 CCGGTGCAAGTGGGGCTTCAACTGGTTCAAGAACGCCGACAAACCGCTCCATGACCTACA 976  
 Db 566 CCGGTGCTACTTGGCGCTTGGACTGGTTCAGAGAACGCCGACAAATCGAGCTTCAGTTCC 625  
 QY 977 AGGAGGTACCTTGGCCCCAAGAGATCAACCGCTTAAGACCGGATGCTCGCGCAA 1028  
 Db 626 GTCAAGTTCAGTGGCGCGGAGCTCGTCCGCTCGCACCGGATGCCCGCGCAA 677

Search completed: June 18, 2003, 02:04:11  
 Job time : 295 secs

Query Match 27.5%; Score 286.4; DB 13; Length 1060;  
 Best Local Similarity 70.7%; Pred. No. 3.5e-48;  
 Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;  
 QY 381 CAGCGCTGTGTCAGCGGTGGCGCTAGCGGC-AACCGCGTCTACTACCGCTACTGGGACTGCT 439  
 Db 47 CCGCCCTGCCGGTGTGGCCCTTGGCGCTGATGGCAGGTCCACCCGCTACTGGGACTGCT 106  
 QY 440 GCAAGGCTTGTGCTGTGGCCCGCAAGGCTAACGTCAGCTCGCCTGTCAAGTCTCTGCA 499  
 Db 107 GCAAGCTTGTGCTGTGGCCCGCAAGGCTCCCGTGAACCAAGCTGTCTTTCTGCA 166  
 QY 500 ACNAGAGCGGCTGTCAGCGCTTTAGGAGCTTCAACGCCAGTCCGGCTGCAA---CGGCG 556  
 Db 167 AC---GCCAACTTCCAGCGGTATCAGCGACTTCAGCGCAAGTCCGGCTCGAGCGGGCG 223

**THIS PAGE BLANK (USPTO)**